



1/20

SGK	²⁵⁶ TTSTFCGTPPEYLAPE..... ⁴²² FLGFSYAPP
PKBα	³⁰⁸ TMKTFCGTPEYLAPE..... ⁴⁷³ FPQFSYSAS
p70 S6K	²²⁹ VTHTFCGTIEYMAPE..... ³⁸⁹ FLGFTYVAP
PKCδ	⁵⁰⁷ RASTFCGTPDYIAPE..... ⁶⁶⁴ FAGFSFVNP

} SEC ID No: 45

Figure 1

$$556 + 0.0017 = 556.0017$$

SE 67-10735

CCGAGTGGACCTGTATGCCCAOCTGGGAACCCCAATTCCA

SECTION: 2 M N B S F A
SECCVCTACGGGAAAGTCTACTG

240 51

[illegible][illegible][illegible][illegible]

CTGAGGCCCGGGCCAGG...
L E P R A R F Y A A E V A B A T
TGCACCTTGACCTTGGCACCTTAGGTGCTTCGCGG

CACGTCGTCGACCGGATTTTGGCCGACAGGCT
 V V V L T D F G L C K E G V E P E D T L E
 TGGCCGCGCCGCTTCTACAGCCAAAGATGTATCCGATGTATGAGAACATTTCTGCACGACGCGCG

[illegible]

CAGATCCCGGAGGCCGGACACTGTGCCTTTCCTCCTCAAGAACC...
- - - - - v l A C D L L Q B L H K D Q R Q R L G U
- - - - - CTCTTGACGTTTTCACCCAGATT

[illegible]

F S P I N V
.....GGGCTATACCCCTCAGCTGTGCCCAACAACCCTCGGCCTCAATTCCTGGGA....
.....TAAAGAGAGAABBAFLQFSGYAPEDDDTL

CAGCATTTTCTTGACGACAT...-..

8 K S I Q C T F L
G G A A G G A A T T A G C C T T C A G C T C T A G G A A G A G G A C T C A A A C T A A C A A G G C C A A A T G G C T T C C A A T T G G C T T A G G C T T T T G C

[illegible]

CCATCTCACTAACCACCCAGCCCACCG...
GTTTGGCATTAGGCCCATGGGTGTCGCCAGTTCTTGAAAAGD

TATOTUAAAAAAAA
SEA ID No: 5
TATOTUAAAAAAAA

M Q O U L T

SEA TO NO: 8

CAGCTTGGGAGCGGGGCGGG

Figure 11

CTCCCTGTTCGCCCGAGGCTGGCTATCATCTTCTACCAATTAATTTGCTC-
 TTTTTPDHCYRMN8

Figure 11

SEE TO NO: 8

SEALED No. 5

CAGCCTGGGACGGG

QOTAGDAAACCTCA

CTCCCTGTCCCCCA

2



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** SEQ ID NO: 4

* SEQ ID NO: 3

SGK2β SEQ ID NO: 8

hSGK1	MTVKTAAAG	TLTYSRMRGM	VAILIAFMKO	RRMGINDPQ	KIANNYSACK
hSGK2	MQGLLTSGRK	PSGGGRCTGR	GGWRGQWCLK	PWMGGAD---	-PPTPTLSCL
mSGK2*					
hSGK3	MALRIFAKRI	FGD-----	-NFDPLFTKO	RRAGLNBFIO	NLVRYPELYN

SGK2α SEQ ID NO: 1

hSGK1	HPVQSLKI	SCQOPELMN	ANPSPPSP-	---S-QQINL	GPSSNPFAKP
hSGK2	LLPVPPPLPD	HCYRMNSSPA	GTPSQPSR	---ANGNINL	GPSANENACP
mSGK2		---MASSPV	GVPSQPSR	---ANGNINL	GPSANENARP
hSGK3	HEDVRAFLQM	DSPKHQSDPS	EDEDERSQK	LHSTSONINL	GPSNPFAKP

hSGK1	SDFEIRLVIG	RGSEGRVLLA	RKNAEEVFYA	VKVLQKRAIL	KRKEBNHTMS
hSGK2	TDDEIRLVIG	RGNYGRVLLA	KRKSDGAFYA	VKVLQKRSIL	KRKEQSHIMA
mSGK2	TDDEIRLVIG	RGNYGRVLLA	KRKSDGAFYA	VKVLQKRSIL	KRKEQSHIMA
hSGK3	TDDEIRLVIG	RGSEGRVLLA	KRKIDGAFYA	VKVLQKRIVL	KRKEQSHIMA

hSGK1	ERNVILKRVK	HEEIVGLHES	FQTADRIVYV	LDYVNGGGEIT	YHLQRPQFL
hSGK2	ERSVILKRVK	HEEIVGDRYS	FQTEERIVYV	LDYVNGGGEIT	PHLQRRSFL
mSGK2	ERNVILKRVK	HEEIVGDRYS	FQTEERIVYV	LDYVNGGGEIT	PHLQRRSFL
hSGK3	ERNVILKRVK	HEEIVGLHES	FQTEERIVYV	LDYVNGGGEIT	PHLQRRSFL

hSGK1	EPRAREYAAE	IASALGYLHS	LNIMYRDLKP	ENILHDSQGH	IVLIDEGGLCK
hSGK2	EPRAREYAAE	VASAIGYLHS	LNILYRDLKP	ENILHDCOGH	VVLIDEGGLCK
mSGK2	EPRAREYAAE	VASAIGYLHS	LNILYRDLKP	ENILHDCOGH	VVLIDEGGLCK
hSGK3	EPRAREYAAE	IASALGYLHS	IKLIVYRDLKP	ENILHDSVGH	VVLIDEGGLCK

*

hSGK1	ENIBHNSITIS	TECGIPEYIA	PEVLKQPYD	RAVENWCIRGA	VLYEMLYGLP
hSGK2	EGVDEENHIS	TECGIPEYIA	PEVLKQPYD	SAVLCWCIRGA	VLYEMHGLP
mSGK2	ECVEPEBITIS	TECGIPEYIA	PEVLKQPYD	RAVENWCIRGA	VLYEMHGLP
hSGK3	EGIAISDITIT	TECGIPEYIA	PEVLKQPYD	NTVDWCIRGA	VLYEMLYGLP

hSGK1	FFYSRNTABM	YDNILNKPLQ	LKPNITNSAR	HLLEGTLQKD	RTKRLGAKDD
hSGK2	FFYSQDVQOM	YENITHQPLQ	IFGGRTVAAC	DLLOSLHKKD	CRORLGSKAD
mSGK2	FFENTLVAQM	YENITHQPLQ	IFGGRTVAAC	DLLOGLHKKD	CRORLGSKED
hSGK3	FFYQDVABM	YDNILNKPLS	LRPGVSLTAW	SLLEBLLKED	RQNRLGAKED

hSGK1	FMELNSHVFF	SLINWDDLIN	KRIIPFFNPN	VSGPNELRHF	DPEETEEVP
hSGK2	FMELNNHVFF	SPINWDDLH	KRIIPFFNPN	VIGPADLKH	DPEETQEAUS
mSGK2	FLDIKNHMF	SPINWDDLH	KRIIPFFNPN	VEGFADLKH	DPEETQEAUS
hSGK3	FLEIQNHFF	ESLSWADLVQ	KRIIPFFNPN	VAGPDIDRNF	DTAETBETVP

*

hSGK1	NSIGKSPDSV	LVTASVKEAA	EAFIGESYAP	ETDSRL--
hSGK2	RSIGCTFDIV	---ASSSCAS	SAELGESYAP	EDDHHHDC
mSGK2	KSIGCTFDIV	---ASSSCAS	SAELGESYAO	EDDHHHDS
hSGK3	YSVCVSSDYS	IVNASVLEAD	DAFVGFSYAP	PSEDLFLL-

Figure 13